

SEQUENCE LISTING

(2) GENERAL INFORMATION:

- (i) APPLICANT: Mosselman, Sieste
Dijkema, Rein
- (ii) TITLE OF INVENTION: Novel estrogen receptor
- (iii) NUMBER OF SEQUENCES: 28
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Akzo Nobel Patent Dept.
 - (B) STREET: 1300 Piccard Drive, Suite 206
 - (C) CITY: Rockville
 - (D) STATE: Maryland
 - (E) COUNTRY: US
 - (F) ZIP: 20850
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/826,361
 - (B) FILING DATE: 26-MAR-1997
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Gormley, Mary E.
 - (B) REGISTRATION NUMBER: 34,409
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 301-948-7400
 - (B) TELEFAX: 301-948-9751

(2) INFORMATION FOR SEQ ID NO: 1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1434 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

ATGAATTACA GCATTCCCAG CAATGTCAC T AACTTGGAAG GTGGGCCTGG TCGGCAGACC	60
ACAAGCCCAA ATGTGTTGTG GCCAACACCT GGGCACCTTT CTCCTTTAGT GGTCCATCGC	120
CAGTTATCAC ATCTGTATGC GGAACCTCAA AAGAGTCCCT GGTGTGAAGC AAGATCGCTA	180
GAACACACCT TACCTGTAAA CAGAGAGACA CTGAAAAGGA AGGTTAGTGG GAACCGTTGC	240
GCCAGCCCTG T TACTGGTCC AGGTTCAAAG AGGGATGCTC ACTTCTGCGC TGTCTGCAGC	300
GATTACGCAT CGGGATATCA CTATGGAGTC TGGTCGTGTG AAGGATGTAA GGCCTTTTTT	360
AAAAGAAGCA TTCAAGGACA TAATGATTAT ATTTGTCCAG CTACAAATCA GTGTACAATC	420
GATAAAAACC GCGCAAGAG CTGCCAGGCC TGCCGACTTC GGAAGTGTTA CGAAGTGGGA	480
ATGGTGAAGT GTGGCTCCCG GAGAGAGAGA TGTGGGTACC GCCTTGTGCG GAGACAGAGA	540
AGTGCCGACG AGCAGCTGCA CTGTGCCGGC AAGGCCAAGA GAAGTGGCGG CCACGCGCCC	600
CGAGTSCGGG AGCTGCTGCT GGACGCCCTG AGCCCCGAGC AGCTAGTGCT CACCCTCCTG	660
GAGGCTGAGC CGCCCCATGT GCTGATCAGC CGCCCCAGTG CGCCCTTCAC CGAGGCCTCC	720
ATGATGATGT CCCTGACCAA GTTGCCCGAC AAGGAGTTGG TACACATGAT CAGCTGGGCC	780
AAGAAGATTC CCGGCTTTGT GGAGCTCAGC CTGTTCCGACC AAGTGCGGCT CTTGGAGAGC	840
TGTTGGATGG AGGTGTTAAT GATGGGGCTG ATGTGGCGCT CAATTGACCA CCCC GGCAAG	900
CTCATCTTTG CTCCAGATCT TGTTCTGGAC AGGGATGAGG GGAAATGCGT AGAAGGAATT	960
CTGGAAATCT TTGACATGCT CCTGGCAACT ACTTCAAGGT TTCGAGAGTT AAAACTCCAA	1020
CACAAAGAAT ATCTCTGTGT CAAGGCCATG ATCCTGCTCA ATTCCAGTAT GTACCCTCTG	1080
GTACACAGCGA CCCAGGATGC TGACAGCAGC CGGAAGCTGG CTCACTTGCT GAACGCCGTG	1140
ACCGATGCTT TGGTTTGGGT GATTGCCAAG AGCGGCATCT CCTCCAGCA GCAATCCATG	1200
CGCCTGGCTA ACCTCCTGAT GCTCCTGTCC CACGTCAGGC ATGCGAGTAA CAAGGGCATG	1260
GAACATCTGC TCAACATGAA GTGCAAAAAT GTGGTCCCAG TGTATGACCT GCTGCTGGAG	1320
ATGCTGAATG CCCACGTGCT TCGCGGGTGC AAGTCCTCCA TCACGGGGTC CGAGTGCAGC	1380
CCGCGCAGAGG ACAGTAAAAG CAAAGAGGGC TCCCAGAACC CACAGTCTCA GTGA	1434

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1251 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

ATGAATTACA GCATTCCCAG CAATGTCACT AACTTGGAAG GTGGGCCTGG TCGGCAGACC	60
ACAAGCCCAA ATGTGTTGTG GCCAACACCT GGGCACCTTT CTCCTTTAGT GGTCCATCGC	120
CAGTTATCAC ATCTGTATGC GGAACCTCAA AAGAGTCCCT GGTGTGAAGC AAGATCGCTA	180
GAACACACCT TACCTGTAAA CAGAGAGACA CTGAAAAGGA AGGTTAGTGG GAACCGTTGC	240
GCCAGCCCTG TTA CTGGTCC AGGTTCAAAG AGGGATGCTC ACTTCTGCGC TGTCTGCAGC	300
GATTACGCAT CGGGATATCA CTATGGAGTC TGGTCGTGTG AAGGATGTAA GGCCTTTTTT	360
AAAAGAAGCA TTCAAGGACA TAATGATTAT ATTTGTCCAG CTACAAATCA GTGTACAATC	420
GATAAAAACC GGC GCAAGAG CTGCCAGGCC TGCCGACTTC GGAAGTGTTA CGAAGTGGGA	480
ATGGTGAAGT GTGGCTCCCG GAGAGAGAGA TGTGGGTACC GCCTTGTGCG GAGACAGAGA	540
AGTGCCGACG AGCAGCTGCA CTGTGCCGGC AAGGCCAAGA GAAGTGGCGG CCACGCGCCC	600
CGAGTGCGGG AGCTGCTGCT GGACGCCCTG AGCCCCGAGC AGCTAGTGCT CACCCTCCTG	660
GAGGCTGAGC CGCCCCATGT GCTGATCAGC CGCCCCAGTG CGCCCTTCAC CGAGGCCTCC	720
ATGATGATGT CCCTGACCAA GTTGGCCGAC AAGGAGTTGG TACACATGAT CAGCTGGGCC	780
AAGAAGATTC CCGGCTTTGT GGAGCTCAGC CTGTTGACC AAGTGCGGCT CTTGGAGAGC	840
TGTTGGATGG AGGTGTTAAT GATGGGGCTG ATGTGGCGCT CAATTGACCA CCCC GGCAAG	900
CTCATCTTTG CTCCAGATCT TGTTCTGGAC AGGGATGAGG GGAAATGCGT AGAAGGAATT	960
CTGGAAATCT TTGACATGCT CCTGGCAACT ACTTCAAGGT TTCGAGAGTT AAAACTCCAA	1020
CACAAAGAAT ATCTCTGTGT CAAGGCCATG ATCCTGCTCA ATTCCAGTAT GTACCCTCTG	1080
GTACAGCGA CCCAGGATGC TGACAGCAGC CGGAAGCTGG CTCACTTGCT GAACGCCGTG	1140

ACCGATGCTT TGGTTTGGGT GATTGCCAAG AGCGGCATCT CCTCCCAGCA GCAATCCATG 1200
 CGCCTGGCTA ACCTCCTGAT GCTCCTGTCC CACGTCAGGC ATGCGAGGTG A 1251

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 66 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Cys	Ala	Val	Cys	Ser	Asp	Tyr	Ala	Ser	Gly	Tyr	His	Tyr	Gly	Val	Trp
1				5					10					15	
Ser	Cys	Glu	Gly	Cys	Lys	Ala	Phe	Phe	Lys	Arg	Ser	Ile	Gln	Gly	His
		20					25						30		
Asn	Asp	Tyr	Ile	Cys	Pro	Ala	Thr	Asn	Gln	Cys	Thr	Ile	Asp	Lys	Asn
		35					40					45			
Arg	Arg	Lys	Ser	Cys	Gln	Ala	Cys	Arg	Leu	Arg	Lys	Cys	Tyr	Glu	Val
	50					55					60				
Gly	Met														
65															

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 233 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Leu	Val	Leu	Thr	Leu	Leu	Glu	Ala	Glu	Pro	Pro	His	Val	Leu	Ile	Ser	1	5	10	15
Arg	Pro	Ser	Ala	Pro	Phe	Thr	Glu	Ala	Ser	Met	Met	Met	Ser	Leu	Thr	20	25	30	
Lys	Leu	Ala	Asp	Lys	Glu	Leu	Val	His	Met	Ile	Ser	Trp	Ala	Lys	Lys	35	40	45	
Ile	Pro	Gly	Phe	Val	Glu	Leu	Ser	Leu	Phe	Asp	Gln	Val	Arg	Leu	Leu	50	55	60	
Glu	Ser	Cys	Trp	Met	Glu	Val	Leu	Met	Met	Gly	Leu	Met	Trp	Arg	Ser	65	70	75	80
Ile	Asp	His	Pro	Gly	Lys	Leu	Ile	Phe	Ala	Pro	Asp	Leu	Val	Leu	Asp	85	90	95	
Arg	Asp	Glu	Gly	Lys	Cys	Val	Glu	Gly	Ile	Leu	Glu	Ile	Phe	Asp	Met	100	105	110	
Leu	Leu	Ala	Thr	Thr	Ser	Arg	Phe	Arg	Glu	Leu	Lys	Leu	Gln	His	Lys	115	120	125	
Glu	Tyr	Leu	Cys	Val	Lys	Ala	Met	Ile	Leu	Leu	Asn	Ser	Ser	Met	Tyr	130	135	140	
Pro	Leu	Val	Thr	Ala	Thr	Gln	Asp	Ala	Asp	Ser	Ser	Arg	Lys	Leu	Ala	145	150	155	160
His	Leu	Leu	Asn	Ala	Val	Thr	Asp	Ala	Leu	Val	Trp	Val	Ile	Ala	Lys	165	170	175	
Ser	Gly	Ile	Ser	Ser	Gln	Gln	Gln	Ser	Met	Arg	Leu	Ala	Asn	Leu	Leu	180	185	190	
Met	Leu	Leu	Ser	His	Val	Arg	His	Ala	Ser	Asn	Lys	Gly	Met	Glu	His	195	200	205	
Leu	Leu	Asn	Met	Lys	Cys	Lys	Asn	Val	Val	Pro	Val	Tyr	Asp	Leu	Leu	210	215	220	
Leu	Glu	Met	Leu	Asn	Ala	His	Val	Leu								225	230		

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

```

Met Asn Tyr Ser Ile Pro Ser Asn Val Thr Asn Leu Glu Gly Gly Pro
 1              5              10              15

Gly Arg Gln Thr Thr Ser Pro Asn Val Leu Trp Pro Thr Pro Gly His
          20              25              30

Leu Ser Pro Leu Val Val His Arg Gln Leu Ser His Leu Tyr Ala Glu
          35              40              45

Pro Gln Lys Ser Pro Trp Cys Glu Ala Arg Ser Leu Glu His Thr Leu
          50              55              60

Pro Val Asn Arg Glu Thr Leu Lys Arg Lys Val Ser Gly Asn Arg Cys
65              70              75              80

Ala Ser Pro Val Thr Gly Pro Gly Ser Lys Arg Asp Ala His Phe Cys
          85              90              95

Ala Val Cys Ser Asp Tyr Ala Ser Gly Tyr His Tyr Gly Val Trp Ser
          100             105             110

Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser Ile Gln Gly His Asn
          115             120             125

Asp Tyr Ile Cys Pro Ala Thr Asn Gln Cys Thr Ile Asp Lys Asn Arg
          130             135             140

Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys Cys Tyr Glu Val Gly
          145             150             155             160

Met Val Lys Cys Gly Ser Arg Arg Glu Arg Cys Gly Tyr Arg Leu Val
          165             170             175

Arg Arg Gln Arg Ser Ala Asp Glu Gln Leu His Cys Ala Gly Lys Ala
          180             185             190

Lys Arg Ser Gly Gly His Ala Pro Arg Val Arg Glu Leu Leu Leu Asp
          195             200             205

```

Ala	Leu	Ser	Pro	Glu	Gln	Leu	Val	Leu	Thr	Leu	Leu	Glu	Ala	Glu	Pro
210						215					220				
Pro	His	Val	Leu	Ile	Ser	Arg	Pro	Ser	Ala	Pro	Phe	Thr	Glu	Ala	Ser
225					230					235					240
Met	Met	Met	Ser	Leu	Thr	Lys	Leu	Ala	Asp	Lys	Glu	Leu	Val	His	Met
				245					250					255	
Ile	Ser	Trp	Ala	Lys	Lys	Ile	Pro	Gly	Phe	Val	Glu	Leu	Ser	Leu	Phe
			260					265					270		
Asp	Gln	Val	Arg	Leu	Leu	Glu	Ser	Cys	Trp	Met	Glu	Val	Leu	Met	Met
		275					280					285			
Gly	Leu	Met	Trp	Arg	Ser	Ile	Asp	His	Pro	Gly	Lys	Leu	Ile	Phe	Ala
	290					295					300				
Pro	Asp	Leu	Val	Leu	Asp	Arg	Asp	Glu	Gly	Lys	Cys	Val	Glu	Gly	Ile
305					310					315					320
Leu	Glu	Ile	Phe	Asp	Met	Leu	Leu	Ala	Thr	Thr	Ser	Arg	Phe	Arg	Glu
				325					330					335	
Leu	Lys	Leu	Gln	His	Lys	Glu	Tyr	Leu	Cys	Val	Lys	Ala	Met	Ile	Leu
			340					345					350		
Leu	Asn	Ser	Ser	Met	Tyr	Pro	Leu	Val	Thr	Ala	Thr	Gln	Asp	Ala	Asp
		355					360					365			
Ser	Ser	Arg	Lys	Leu	Ala	His	Leu	Leu	Asn	Ala	Val	Thr	Asp	Ala	Leu
	370					375					380				
Val	Trp	Val	Ile	Ala	Lys	Ser	Gly	Ile	Ser	Ser	Gln	Gln	Gln	Ser	Met
385					390					395					400
Arg	Leu	Ala	Asn	Leu	Leu	Met	Leu	Leu	Ser	His	Val	Arg	His	Ala	Ser
				405					410					415	
Asn	Lys	Gly	Met	Glu	His	Leu	Leu	Asn	Met	Lys	Cys	Lys	Asn	Val	Val
			420					425					430		
Pro	Val	Tyr	Asp	Leu	Leu	Leu	Glu	Met	Leu	Asn	Ala	His	Val	Leu	Arg
		435					440					445			
Gly	Cys	Lys	Ser	Ser	Ile	Thr	Gly	Ser	Glu	Cys	Ser	Pro	Ala	Glu	Asp
	450					455					460				
Ser	Lys	Ser	Lys	Glu	Gly	Ser	Gln	Asn	Pro	Gln	Ser	Gln			
465					470					475					

2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

```

Met Asn Tyr Ser Ile Pro Ser Asn Val Thr Asn Leu Glu Gly Gly Pro
1           5           10           15

Gly Arg Gln Thr Thr Ser Pro Asn Val Leu Trp Pro Thr Pro Gly His
          20           25           30

Leu Ser Pro Leu Val Val His Arg Gln Leu Ser His Leu Tyr Ala Glu
          35           40           45

Pro Gln Lys Ser Pro Trp Cys Glu Ala Arg Ser Leu Glu His Thr Leu
          50           55           60

Pro Val Asn Arg Glu Thr Leu Lys Arg Lys Val Ser Gly Asn Arg Cys
65           70           75           80

Ala Ser Pro Val Thr Gly Pro Gly Ser Lys Arg Asp Ala His Phe Cys
          85           90           95

Ala Val Cys Ser Asp Tyr Ala Ser Gly Tyr His Tyr Gly Val Trp Ser
          100          105          110

Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser Ile Gln Gly His Asn
          115          120          125

Asp Tyr Ile Cys Pro Ala Thr Asn Gln Cys Thr Ile Asp Lys Asn Arg
          130          135          140

Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys Cys Tyr Glu Val Gly
          145          150          155          160

Met Val Lys Cys Gly Ser Arg Arg Glu Arg Cys Gly Tyr Arg Leu Val
          165          170          175

Arg Arg Gln Arg Ser Ala Asp Glu Gln Leu His Cys Ala Gly Lys Ala
          180          185          190

Lys Arg Ser Gly Gly His Ala Pro Arg Val Arg Glu Leu Leu Leu Asp
          195          200          205

```


Ala	Leu	Ser	Pro	Glu	Gln	Leu	Val	Leu	Thr	Leu	Leu	Glu	Ala	Glu	Pro
210						215					220				
Pro	His	Val	Leu	Ile	Ser	Arg	Pro	Ser	Ala	Pro	Phe	Thr	Glu	Ala	Ser
225					230					235					240
Met	Met	Met	Ser	Leu	Thr	Lys	Leu	Ala	Asp	Lys	Glu	Leu	Val	His	Met
			245						250					255	
Ile	Ser	Trp	Ala	Lys	Lys	Ile	Pro	Gly	Phe	Val	Glu	Leu	Ser	Leu	Phe
			260					265					270		
Asp	Gln	Val	Arg	Leu	Leu	Glu	Ser	Cys	Trp	Met	Glu	Val	Leu	Met	Met
		275					280					285			
Gly	Leu	Met	Trp	Arg	Ser	Ile	Asp	His	Pro	Gly	Lys	Leu	Ile	Phe	Ala
290						295					300				
Pro	Asp	Leu	Val	Leu	Asp	Arg	Asp	Glu	Gly	Lys	Cys	Val	Glu	Gly	Ile
305					310					315					320
Leu	Glu	Ile	Phe	Asp	Met	Leu	Leu	Ala	Thr	Thr	Ser	Arg	Phe	Arg	Glu
				325					330					335	
Leu	Lys	Leu	Gln	His	Lys	Glu	Tyr	Leu	Cys	Val	Lys	Ala	Met	Ile	Leu
			340					345					350		
Leu	Asn	Ser	Ser	Met	Tyr	Pro	Leu	Val	Thr	Ala	Thr	Gln	Asp	Ala	Asp
		355					360					365			
Ser	Ser	Arg	Lys	Leu	Ala	His	Leu	Leu	Asn	Ala	Val	Thr	Asp	Ala	Leu
		370				375					380				
Val	Trp	Val	Ile	Ala	Lys	Ser	Gly	Ile	Ser	Ser	Gln	Gln	Gln	Ser	Met
385					390					395					400
Arg	Leu	Ala	Asn	Leu	Leu	Met	Leu	Leu	Ser	His	Val	Arg	His	Ala	Arg
			405						410					415	

(2) INFORMATION FOR SEQ ID NO: 7:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 29 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

GGIGAYGARG CWTGIGGITG YCAYTAYGG

29

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

AAGCCTGGS A YICKYTTIG C CCAIYTIAT

29

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TGTTACGAAG TGGGAATGGT GA

22

(2) INFORMATION FOR SEQ ID NO: 10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

TTGACACCAG ACCAACTGGT AATG

24

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

GGTGGCGACG ACTCCTGGAG CCCG

24

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 22 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

GTACACTGAT TTGTAGCTGG AC

22

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CCATGATGAT GTCCCTGACC

20

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

TGGCATGCCT GACGTGGGAC

20

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GCGSTCCAGC ATCTCCAGSA RCAG

24

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

GGAAGCTGGC TCACTTGCTG

20

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

TCTTGTTCTG GACAGGGATG

20

(2) INFORMATION FOR SEQ ID NO: 18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

GCATGGAACA TCTGCTCAAC

20

(2) INFORMATION FOR SEQ ID NO: 19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 21 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

AGCAAGTTCA GCCTGTTAAG T

21

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1257 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

ATGAATTACA GCATTCCCAG CAATGTCAC T AACTTGGAAG GTGGGCCTGG TCGGCAGACC	60
ACAAGCCCAA ATGTGTTGTG GCCAACACCT GGGCACCTTT CTCCTTTAGT GGTCCATCGC	120
CAGTTATCAC ATCTGTATGC GGAACCTCAA AAGAGTCCCT GGTGTGAAGC AAGATCGCTA	180
GAACACACCT TACCTGTAAA CAGAGAGACA CTGAAAAGGA AGGTTAGTGG GAACCGTTGC	240
GCCAGCCCTG TTA CTGGTCC AGGTTCAAAG AGGGATGCTC ACTTCTGCGC TGTCTGCAGC	300
GATTACGCAT CGGGATATCA CTATGGAGTC TGGTCGTGTG AAGGATGTAA GGCCTTTTTT	360
AAAAGAAGCA TTCAAGGACA TAATGATTAT ATTTGTCCAG CTACAAATCA GTGTACAATC	420
GATAAAAACC GGCGCAAGAG CTGCCAGGCC TGCCGACTTC GGAAGTGTTA CGAAGTGGGA	480
ATGGTGAAGT GTGGCTCCCG GAGAGAGAGA TGTGGGTACC GCCTTGTGCG GAGACAGAGA	540
AGTGCCGACG AGCAGCTGCA CTGTGCCGGC AAGGCCAAGA GAAGTGGCGG CCACGCGCCC	600
CGAGTGCGGG AGCTGCTGCT GGACGCCCTG AGCCCCGAGC AGCTAGTGCT CACCCTCCTG	660
GAGGCTGAGC CGCCCCATGT GCTGATCAGC CGCCCCAGTG CGCCCTTCAC CGAGGCCTCC	720
ATGATGATGT CCCTGACCAA GTTGGCCGAC AAGGAGTTGG TACACATGAT CAGCTGGGCC	780
AAGAAGATTC CCGGCTTTGT GGAGCTCAGC CTGTTCGACC AAGTGCGGCT CTTGGAGAGC	840
TGTTGGATGG AGGTGTTAAT GATGGGGCTG ATGTGGCGCT CAATTGACCA CCCC GGCAAG	900
CTCATCTTTG CTCCAGATCT TGTTCTGGAC AGGGATGAGG GGAAATGCGT AGAAGGAATT	960
CTGGAAATCT TTGACATGCT CCTGGCAACT ACTTCAAGGT TTCGAGAGTT AAAACTCCAA	1020
CACAAAGAAT ATCTCTGTGT CAAGGCCATG ATCCTGCTCA ATTCCAGTAT GTACCCTCTG	1080
CTCACAGCGA CCCAGGATGC TGACAGCAGC CGGAAGCTGG CTCACTTGCT GAACGCCGTG	1140

ACCGATGCTT TGATTGGGT GATTGCCAAG AGCGGCATCT CCTCCCAGCA GCAATCCATG 1200
 CGCCTGGCTA ACCTCCTGAT GCTCCTGTCC CACGTCAGGC ATGCGAGGTC TGCCTGA 1257

(2) INFORMATION FOR SEQ ID NO: 21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

Met	Asn	Tyr	Ser	Ile	Pro	Ser	Asn	Val	Thr	Asn	Leu	Glu	Gly	Gly	Pro
1				5					10					15	
Gly	Arg	Gln	Thr	Thr	Ser	Pro	Asn	Val	Leu	Trp	Pro	Thr	Pro	Gly	His
			20					25					30		
Leu	Ser	Pro	Leu	Val	Val	His	Arg	Gln	Leu	Ser	His	Leu	Tyr	Ala	Glu
		35					40					45			
Pro	Gln	Lys	Ser	Pro	Trp	Cys	Glu	Ala	Arg	Ser	Leu	Glu	His	Thr	Leu
	50					55					60				
Pro	Val	Asn	Arg	Glu	Thr	Leu	Lys	Arg	Lys	Val	Ser	Gly	Asn	Arg	Cys
65					70					75					80
Ala	Ser	Pro	Val	Thr	Gly	Pro	Gly	Ser	Lys	Arg	Asp	Ala	His	Phe	Cys
				85					90					95	
Ala	Val	Cys	Ser	Asp	Tyr	Ala	Ser	Gly	Tyr	His	Tyr	Gly	Val	Trp	Ser
			100					105					110		
Cys	Glu	Gly	Cys	Lys	Ala	Phe	Phe	Lys	Arg	Ser	Ile	Gln	Gly	His	Asn
		115					120					125			
Asp	Tyr	Ile	Cys	Pro	Ala	Thr	Asn	Gln	Cys	Thr	Ile	Asp	Lys	Asn	Arg
	130					135					140				
Arg	Lys	Ser	Cys	Gln	Ala	Cys	Arg	Leu	Arg	Lys	Cys	Tyr	Glu	Val	Gly
145					150					155					160
Met	Val	Lys	Cys	Gly	Ser	Arg	Arg	Glu	Arg	Cys	Gly	Tyr	Arg	Leu	Val
				165					170					175	

[illegible]

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

CTTGGATCCA TAGCCCTGCT GTGATGAATT ACAG

34

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

GATGGATCCT CACCTCAGGG CCAGGCGTCA CTG

33

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1898 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

CACGAATCTT TGAGAACATT ATAATGACCT TTGTGCCTCT TCTTGCAAGG TGTTTTCTCA

60

GCTGTTATCT CAAGACATGG ATATAAAAAA CTCACCATCT AGCCTTAATT CTCCTTCCTC

120

CTACAACTGC AGTCAATCCA TCTTACCCCT GGAGCACGGC TCCATATACA TACCTTCCTC

180

CTATGTAGAC	AGCCACCATG	AATATCCAGC	CATGACATTC	TATAGCCCTG	CTGTGATGAA	240
TTACAGCATT	CCCAGCAATG	TCACTAACTT	GGAAGGTGGG	CCTGGTCGGC	AGACCACAAG	300
CCCAAATGTG	TTGTGGCCAA	CACCTGGGCA	CCTTTCTCCT	TTAGTGGTCC	ATCGCCAGTT	360
ATCACATCTG	TATGCGGAAC	CTCAAAGAG	TCCCTGGTGT	GAAGCAAGAT	CGCTAGAACA	420
CACCTTACCT	GTAAACAGAG	AGACACTGAA	AAGGAAGGTT	AGTGGGAACC	GTTGCGCCAG	480
CCCTGTTACT	GGTCCAGGTT	CAAAGAGGGA	TGCTCACTTC	TGCGCTGTCT	GCAGCGATTA	540
CGCATCGGGA	TATCACTATG	GAGTCTGGTC	GTGTGAAGGA	TGTAAGGCCT	TTTTTAAAAG	600
AAGCATTCAA	GGACATAATG	ATTATATTTG	TCCAGCTACA	AATCAGTGTA	CAATCGATAA	660
AAACCGGCGC	AAGAGCTGCC	AGGCCTGCCG	ACTTCGGAAG	TGTTACGAAG	TGGGAATGGT	720
GAAGTGTGGC	TCCCGGAGAG	AGAGATGTGG	GTACCGCCTT	GTGCGGAGAC	AGAGAAGTGC	780
CGAAGAGCAG	CTGCACTGTG	CCGGCAAGGC	CAAGAGAAGT	GGCGGCCACG	CGCCCCGAGT	840
GCGGGAGCTG	CTGCTGGACG	CCCTGAGCCC	CGAGCAGCTA	GTGCTCACCC	TCCTGGAGGC	900
TGAGCCGCCC	CATGTGCTGA	TCAGCCGCCC	CAGTGCGCCC	TTCACCGAGG	CCTCCATGAT	960
GATGTCCCTG	ACCAAGTTGG	CCGACAAGGA	GTTGGTACAC	ATGATCAGCT	GGGCCAAGAA	1020
GATTCCCGGC	TTTGTGGAGC	TCAGCCTGTT	CGACCAAGTG	CGGCTCTTGG	AGAGCTGTTG	1080
GATGGAGGTG	TTAATGATGG	GGCTGATGTG	GCGCTCAATT	GACCACCCCG	GCAAGCTCAT	1140
CTTTGCTCCA	GATCTTGTTT	TGGACAGGGA	TGAGGGGAAA	TGCGTAGAAG	GAATTCTGGA	1200
AATCTTTGAC	ATGCTCCTGG	CAACTACTTC	AAGGTTTCGA	GAGTTAAAAC	TCCAACACAA	1260
AGAATATCTC	TGTGTCAAGG	CCATGATCCT	GCTCAATTCC	AGTATGTACC	CTCTGGTCAC	1320
AGCGACCCAG	GATGCTGACA	GCAGCCGGAA	GCTGGCTCAC	TTGCTGAACG	CCGTGACCGA	1380
TGCTTTGGTT	TGGGTGATTG	CCAAGAGCGG	CATCTCCTCC	CAGCAGCAAT	CCATGCGCCT	1440
GGCTAACCTC	CTGATGCTCC	TGTCCCACGT	CAGGCATGCG	AGTAACAAGG	GCATGGAACA	1500
TCTGCTCAAC	ATGAAGTGCA	AAAATGTGGT	CCCAGTGTAT	GACCTGCTGC	TGGAGATGCT	1560
GAATGCCCAC	GTGCTTCGCG	GGTGCAAGTC	CTCCATCACG	GGGTCCGAGT	GCAGCCCGGC	1620
AGAGGACAGT	AAAAGCAAAG	AGGGCTCCCA	GAACCCACAG	TCTCAGTGAC	GCCTGGCCCT	1680
GAGGTGAACT	GGCCACAGA	GGTCACAAGC	TGAAGCGTGA	ACTCCAGTGT	GTCAGGAGCC	1740

TGGGCTTCAT CTTTCTGCTG TGTGGTCCCT CATTTGGTGA TGGCAGGCTT GGTCATGTAC 1800
 CATCCTTCCC TCCACCTTCC CAACTCTCAG GAGTCGGTGT GAGGAAGCCA TAGTTTCCCT 1860
 TGTTAGCAGA GGGACATTTG AATCGAGCGT TTCCACAC 1898

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 530 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Met	Asp	Ile	Lys	Asn	Ser	Pro	Ser	Ser	Leu	Asn	Ser	Pro	Ser	Ser	Tyr	1	5	10	15
Asn	Cys	Ser	Gln	Ser	Ile	Leu	Pro	Leu	Glu	His	Gly	Ser	Ile	Tyr	Ile	20	25	30	
Pro	Ser	Ser	Tyr	Val	Asp	Ser	His	His	Glu	Tyr	Pro	Ala	Met	Thr	Phe	35	40	45	
Tyr	Ser	Pro	Ala	Val	Met	Asn	Tyr	Ser	Ile	Pro	Ser	Asn	Val	Thr	Asn	50	55	60	
Leu	Glu	Gly	Gly	Pro	Gly	Arg	Gln	Thr	Thr	Ser	Pro	Asn	Val	Leu	Trp	65	70	75	80
Pro	Thr	Pro	Gly	His	Leu	Ser	Pro	Leu	Val	Val	His	Arg	Gln	Leu	Ser	85	90	95	
His	Leu	Tyr	Ala	Glu	Pro	Gln	Lys	Ser	Pro	Trp	Cys	Glu	Ala	Arg	Ser	100	105	110	
Leu	Glu	His	Thr	Leu	Pro	Val	Asn	Arg	Glu	Thr	Leu	Lys	Arg	Lys	Val	115	120	125	
Ser	Gly	Asn	Arg	Cys	Ala	Ser	Pro	Val	Thr	Gly	Pro	Gly	Ser	Lys	Arg	130	135	140	
Asp	Ala	His	Phe	Cys	Ala	Val	Cys	Ser	Asp	Tyr	Ala	Ser	Gly	Tyr	His	145	150	155	160

Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser
 165 170 175
 Ile Gln Gly His Asn Asp Tyr Ile Cys Pro Ala Thr Asn Gln Cys Thr
 180 185 190
 Ile Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys
 195 200 205
 Cys Tyr Glu Val Gly Met Val Lys Cys Gly Ser Arg Arg Glu Arg Cys
 210 215 220
 Gly Tyr Arg Leu Val Arg Arg Gln Arg Ser Ala Asp Glu Gln Leu His
 225 230 235 240
 Cys Ala Gly Lys Ala Lys Arg Ser Gly Gly His Ala Pro Arg Val Arg
 245 250 255
 Glu Leu Leu Leu Asp Ala Leu Ser Pro Glu Gln Leu Val Leu Thr Leu
 260 265 270
 Leu Glu Ala Glu Pro Pro His Val Leu Ile Ser Arg Pro Ser Ala Pro
 275 280 285
 Phe Thr Glu Ala Ser Met Met Met Ser Leu Thr Lys Leu Ala Asp Lys
 290 295 300
 Glu Leu Val His Met Ile Ser Trp Ala Lys Lys Ile Pro Gly Phe Val
 305 310 315 320
 Glu Leu Ser Leu Phe Asp Gln Val Arg Leu Leu Glu Ser Cys Trp Met
 325 330 335
 Glu Val Leu Met Met Gly Leu Met Trp Arg Ser Ile Asp His Pro Gly
 340 345 350
 Lys Leu Ile Phe Ala Pro Asp Leu Val Leu Asp Arg Asp Glu Gly Lys
 355 360 365
 Cys Val Glu Gly Ile Leu Glu Ile Phe Asp Met Leu Leu Ala Thr Thr
 370 375 380
 Ser Arg Phe Arg Glu Leu Lys Leu Gln His Lys Glu Tyr Leu Cys Val
 385 390 395 400
 Lys Ala Met Ile Leu Leu Asn Ser Ser Met Tyr Pro Leu Val Thr Ala
 405 410 415
 Thr Gln Asp Ala Asp Ser Ser Arg Lys Leu Ala His Leu Leu Asn Ala
 420 425 430

Val Thr Asp Ala Leu Val Trp Val Ile Ala Lys Ser Gly Ile Ser Ser
 435 440 445

Gln Gln Gln Ser Met Arg Leu Ala Asn Leu Leu Met Leu Leu Ser His
 450 455 460

Val Arg His Ala Ser Asn Lys Gly Met Glu His Leu Leu Asn Met Lys
 465 470 475 480

Cys Lys Asn Val Val Pro Val Tyr Asp Leu Leu Leu Glu Met Leu Asn
 485 490 495

Ala His Val Leu Arg Gly Cys Lys Ser Ser Ile Thr Gly Ser Glu Cys
 500 505 510

Ser Pro Ala Glu Asp Ser Lys Ser Lys Glu Gly Ser Gln Asn Pro Gln
 515 520 525

Ser Gln
 530

(2) INFORMATION FOR SEQ ID NO: 26:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

GTGCGGATCC TCTCAAGACA TGGATATAAA

30

(2) INFORMATION FOR SEQ ID NO: 27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 25 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

AGTAACAGGG CTGGCGCAAC GTTTC

25

(2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

ACTGGCGATG GACCACTAAA GG

22